



SEQUENCE LISTING

<110> Joshua Z. Levin
Ken Phillips
Greg Budziszewski
Fred Meins
Zhenya Glazov

<120> Methods of Controlling Gene Expression

<130> PB/5-31481A

<140>

<141>

<160> 38

<170> PatentIn Ver. 2.1

<210> 1

<211> 942

<212> DNA

<213> *Arabidopsis thaliana*

<400> 1

atgtcatcggt	caaattggat	cgacgacgct	tttacagagg	aagagcttct	cgctatcgac	60
gccatcgaaag	cttcctacaa	tttctcccggt	tcttcttctt	cttcttcctc	tgctgctccg	120
accgtacaag	ctacaacctc	cgtccatggc	cacgaggagg	atccaaatca	aatccccaaat	180
aatatccgtc	gccaattgcc	tcgttccatc	acttcttcta	catcttataa	acgatttcct	240
ctctcccggt	gccgagctag	gaattttcca	gcaatgagggt	ttgggtggtag	gattttgttat	300
agcaagactg	ctactgaggt	tgataagcga	gcaatgcagc	ttattaaagt	tcttgatacc	360
aagagagatg	aatctggaat	agctttgtt	ggcttggata	ttgagtggag	accaagttt	420
agaaaagggtg	ttctcccggg	gaaggttgcg	actgtccaga	tatgtgtaga	tagtaattat	480
tgtgatgtta	tgcatatttt	tcattctgggt	atccctcaaa	gtctccaaca	tcttattgaa	540
gattcaacac	ttgtaaaggt	aggtatttgg	attgatgggt	actctgtgaa	gctttccat	600
gactatggag	tttagtatcaa	agatgttgag	gatcttcag	atttagccaa	ccaaaaaaatt	660
ggtggagata	aaaaaatgggg	ccttgcctca	ctaactgaga	cacttgtttg	caaagagctc	720
ctgaagccaa	acagaatcag	gcttggaaac	tgggagtttt	atcctctgtc	aaagcagcag	780
ttacaatacg	cagcaacgg	tgcttatgtct	tcatggcattc	tttacaaggt	aacaacaacg	840
aaaaaccatc	tttcacact	caacgacatt	gaagcaaaaa	tctcacatcg	ttctaattat	900
aatactgtta	cttgtcgaaa	acctggaggt	tatcttcgggt	ga		942

<210> 2

<211> 313

<212> PRT

<213> *Arabidopsis thaliana*

<400> 2

Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
1 5 10 15

Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
 20 25 30

Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
35 40 45

His	Gly	His	Glu	Glu	Asp	Pro	Asn	Gln	Ile	Pro	Asn	Asn	Ile	Arg	Arg
50															
Gln	Leu	Pro	Arg	Ser	Ile	Thr	Ser	Ser	Thr	Ser	Tyr	Lys	Arg	Phe	Pro
65															
Leu	Ser	Arg	Cys	Arg	Ala	Arg	Asn	Phe	Pro	Ala	Met	Arg	Phe	Gly	Gly
85															
Arg	Ile	Leu	Tyr	Ser	Lys	Thr	Ala	Thr	Glu	Val	Asp	Lys	Arg	Ala	Met
100															
Gln	Leu	Ile	Lys	Val	Leu	Asp	Thr	Lys	Arg	Asp	Glu	Ser	Gly	Ile	Ala
115															
Phe	Val	Gly	Leu	Asp	Ile	Glu	Trp	Arg	Pro	Ser	Phe	Arg	Lys	Gly	Val
130															
Leu	Pro	Gly	Lys	Val	Ala	Thr	Val	Gln	Ile	Cys	Val	Asp	Ser	Asn	Tyr
145															
Cys	Asp	Val	Met	His	Ile	Phe	His	Ser	Gly	Ile	Pro	Gln	Ser	Leu	Gln
165															
His	Leu	Ile	Glu	Asp	Ser	Thr	Leu	Val	Lys	Val	Gly	Ile	Gly	Ile	Asp
180															
Gly	Asp	Ser	Val	Lys	Leu	Phe	His	Asp	Tyr	Gly	Val	Ser	Ile	Lys	Asp
195															
Val	Glu	Asp	Leu	Ser	Asp	Leu	Ala	Asn	Gln	Lys	Ile	Gly	Gly	Asp	Lys
210															
Lys	Trp	Gly	Leu	Ala	Ser	Leu	Thr	Glu	Thr	Leu	Val	Cys	Lys	Glu	Leu
225															
230															
235															
240															
Leu	Lys	Pro	Asn	Arg	Ile	Arg	Leu	Gly	Asn	Trp	Glu	Phe	Tyr	Pro	Leu
245															
250															
255															
Ser	Lys	Gln	Gln	Leu	Gln	Tyr	Ala	Ala	Thr	Asp	Ala	Tyr	Ala	Ser	Trp
260															
265															
270															
His	Leu	Tyr	Lys	Val	Thr	Thr	Lys	Asn	His	Leu	Leu	Thr	Leu	Asn	
275															
280															
285															
Asp	Leu	Glu	Ala	Lys	Ile	Ser	His	Arg	Ser	Asn	Tyr	Asn	Thr	Val	Thr
290															
295															
300															
Cys	Arg	Lys	Pro	Gly	Gly	Tyr	Leu	Arg							
305															
310															

<210> 3
 <211> 1929
 <212> DNA
 <213> Arabidopsis thaliana

<400> 3

atgagattt atgatccat ggatgagttc aagaggaatc gaaagatgga ggaagattcg 60
aagaaggtaa tcgatgtgaa agtggctgag agtgataagg gattcgcgaa atttggcaag 120
gcagaggttc cgtttcatat accgacgtta acgaagcctc aagaggagta taagattttg 180
gtagacaatg ctaataatcc tttgagcat gtttggatgg agaagagtga agacggctt 240
cggttcatcc atccactgga ggaactatct gtgatggact ttggtgatag aaatctaagt 300
gagatgagac ctgttaagcc tctcccattt gaagagactc cattcaagct agttgaagaa 360
gtcaaagatc ttgaggactt agctgctgca ttgcaaagtg ttgaagagtt tgctgtcgat 420
ctggagcata atcagtatag aactttcaa ggattaacat gttgatgca aatctctact 480
agaaccgagg attatattgt tgatataattc aagctttggg atcacattgg tccttatcta 540
aggaactct tcaaagaccc taaaaagaaa aaggtaatcc atggagcaga tcgagatatt 600
atttggcttc aacgggactt tggcatttt gtctgcaatc ttttgacac aggacaggct 660
tcaagggtgc taaagctgga gagaatagt ctgaaatttc ttctgaagca ttattgtgga 720
gttgctgcaa acaaagaata ccaaaaagca gactggagaa taagaccctt tccagatgt 780
atgaaaagat atgcttagaga agatacacat tatctttgt acattttatga tgtaatgcga 840
atggagttgc acacaatggc aaaggaagat gagcaatctg actctcctct ggttagaggtg 900
tacaagcgc gttatgacgt gtgcattgca ctatatgaaa aagagctttg gactaggat 960
tcatatcttc acgtttatgg ggttcagaca ggtaatctca atgcgggtca actttccatt 1020
gttgcgctgc aggggctttt tgaatggcg gatcgattt cacgcgcaga tgatgagagc 1080
accggttatg tattgccaaa taaaactctt tttgacatag ccaaggagat gccaattgtt 1140
gttgcggcgt tgcggcgtt gttgaagtca aagcttcattt acctcgagcg taattttgac 1200
gcagtgtca gtgtcatcag acgtcaatg caaatgcag cggcattcga gccagttgtt 1260
caatcttga aagataggcg tcctgaaaca gtggttgaaa tgaatataga acctaagatt 1320
gaaaaaacag acacaggagc ttcaagcgtt tctctgagtc tggagaagggt ttgtgtggat 1380
gattcaaaga aacaaggcag tggttttgga gttttgccgt taaagaggaa gttggaaagt 1440
gacaaaacgg tggttgaaaaa gaatatcgaa cctaagattt agaaaacagg cacagaagct 1500
tcagcttctt ctctgagttc gaagaaggattt tggatggatg attcaaagaa acaaaggcgt 1560
ggtttggag ttttgcgtc aaagaggaag tttgaaagtg ataacaagaa gttgcaggta 1620
aaagaagagg tcaaagtgtc caagtccaaag ccagataagg taatcatagt ggtggatgt 1680
gatgatgatg atgatgatga ttagtctttaatgatgatgatgatgatgatgatgatgatg 1740
gacagagttt cggaaacgccc ttcaagggta tcaccatcg tggatcaaaa gccgaagaca 1800
tgtaatacag aggttattttt gtttagacgt gatgatgact cggaaaggcag agaagatgaa 1860
gacatgcgtt ggagaagtga gaaacatagg agattcatga atatgaaacg tggctttctt 1920
aacattttag 1929

<210> 4

<211> 642

<212> PRT

<213> *Arabidopsis thaliana*

<400> 4

Met Arg Phe Asp Asp Pro Met Asp Glu Phe Lys Arg Asn Arg Lys Met
1 5 10 15

Glu Glu Asp Ser Lys Lys Val Ile Asp Val Lys Val Ala Glu Ser Asp
20 25 30

Lys Gly Phe Ala Lys Phe Gly Lys Ala Glu Val Pro Phe His Ile Pro
35 40 45

Thr Leu Thr Lys Pro Gln Glu Glu Tyr Lys Ile Leu Val Asp Asn Ala
50 55 60

Asn Asn Pro Phe Glu His Val Leu Leu Glu Lys Ser Glu Asp Gly Leu
65 70 75 80

Arg	Phe	Ile	His	Pro	Leu	Glu	Glu	Leu	Ser	Val	Met	Asp	Phe	Val	Asp
				85					90				95		
Arg	Asn	Leu	Ser	Glu	Met	Arg	Pro	Val	Lys	Pro	Leu	Pro	Leu	Glu	Glu
				100				105				110			
Thr	Pro	Phe	Lys	Leu	Val	Glu	Glu	Val	Lys	Asp	Leu	Glu	Asp	Leu	Ala
				115				120				125			
Ala	Ala	Leu	Gln	Ser	Val	Glu	Glu	Phe	Ala	Val	Asp	Leu	Glu	His	Asn
				130				135				140			
Gln	Tyr	Arg	Thr	Phe	Gln	Gly	Leu	Thr	Cys	Leu	Met	Gln	Ile	Ser	Thr
				145				150				155			160
Arg	Thr	Glu	Asp	Tyr	Ile	Val	Asp	Ile	Phe	Lys	Leu	Trp	Asp	His	Ile
				165				170				175			
Gly	Pro	Tyr	Leu	Arg	Glu	Leu	Phe	Lys	Asp	Pro	Lys	Lys	Lys	Val	
				180				185				190			
Ile	His	Gly	Ala	Asp	Arg	Asp	Ile	Ile	Trp	Leu	Gln	Arg	Asp	Phe	Gly
				195				200				205			
Ile	Tyr	Val	Cys	Asn	Leu	Phe	Asp	Thr	Gly	Gln	Ala	Ser	Arg	Val	Leu
				210				215				220			
Lys	Leu	Glu	Arg	Asn	Ser	Leu	Glu	Phe	Leu	Leu	Lys	His	Tyr	Cys	Gly
				225				230				235			240
Val	Ala	Ala	Asn	Lys	Glu	Tyr	Gln	Lys	Ala	Asp	Trp	Arg	Ile	Arg	Pro
				245				250				255			
Leu	Pro	Asp	Val	Met	Lys	Arg	Tyr	Ala	Arg	Glu	Asp	Thr	His	Tyr	Leu
				260				265				270			
Leu	Tyr	Ile	Tyr	Asp	Val	Met	Arg	Met	Glu	Leu	His	Thr	Met	Ala	Lys
				275				280				285			
Glu	Asp	Glu	Gln	Ser	Asp	Ser	Pro	Leu	Val	Glu	Val	Tyr	Lys	Arg	Ser
				290				295				300			
Tyr	Asp	Val	Cys	Met	Gln	Leu	Tyr	Glu	Lys	Glu	Leu	Trp	Thr	Arg	Asp
				305				310				315			320
Ser	Tyr	Leu	His	Val	Tyr	Gly	Val	Gln	Thr	Gly	Asn	Leu	Asn	Ala	Val
				325				330				335			
Gln	Leu	Ser	Ile	Val	Ala	Leu	Gln	Gly	Leu	Cys	Glu	Trp	Arg	Asp	Arg
				340				345				350			
Ile	Ala	Arg	Ala	Asp	Asp	Glu	Ser	Thr	Gly	Tyr	Val	Leu	Pro	Asn	Lys
				355				360				365			
Thr	Leu	Phe	Asp	Ile	Ala	Lys	Glu	Met	Pro	Ile	Val	Val	Ala	Gln	Leu
				370				375				380			

Arg Arg Leu Leu Lys Ser Lys Leu Pro Tyr Leu Glu Arg Asn Phe Asp
 385 390 395 400
 Ala Val Ile Ser Val Ile Arg Arg Ser Met Gln Asn Ala Ala Ala Phe
 405 410 415
 Glu Pro Val Val Gln Ser Leu Lys Asp Arg Arg Pro Glu Thr Val Val
 420 425 430
 Glu Met Asn Ile Glu Pro Lys Ile Glu Lys Thr Asp Thr Gly Ala Ser
 435 440 445
 Ala Ser Ser Leu Ser Leu Glu Lys Val Cys Val Asp Asp Ser Lys Lys
 450 455 460
 Gln Ser Ser Gly Phe Gly Val Leu Pro Leu Lys Arg Lys Leu Glu Ser
 465 470 475 480
 Asp Lys Thr Val Val Glu Lys Asn Ile Glu Pro Lys Ile Glu Lys Thr
 485 490 495
 Gly Thr Glu Ala Ser Ala Ser Ser Leu Ser Ser Lys Lys Val Cys Val
 500 505 510
 Asp Asp Ser Lys Lys Gln Ser Ser Gly Phe Gly Val Leu Leu Ser Lys
 515 520 525
 Arg Lys Phe Glu Ser Asp Asn Lys Lys Leu Gln Val Lys Glu Glu Val
 530 535 540
 Lys Val Ser Lys Ser Lys Pro Asp Lys Val Ile Ile Val Val Asp Asp
 545 550 555 560
 Asp Asp Asp Asp Asp Asp Glu Ser Tyr Glu Gln Ser Thr Lys Ala
 565 570 575
 Ala Asp Ala Leu Asp Arg Val Ser Glu Thr Pro Ser Lys Gly Ser Pro
 580 585 590
 Ser Leu Thr Gln Lys Pro Lys Thr Cys Asn Thr Glu Val Ile Val Leu
 595 600 605
 Asp Asp Asp Asp Asp Ser Glu Ser Arg Glu Asp Glu Asp Met Arg Arg
 610 615 620
 Arg Ser Glu Lys His Arg Arg Phe Met Asn Met Lys Arg Gly Phe Leu
 625 630 635 640
 Asn Ile

<210> 5
 <211> 714
 <212> DNA
 <213> Arabidopsis thaliana

<400> 5

atgaatttgc attttgcattt ttgggtgttt atatttggaaa ctaatgcaga gaaacccctcg 60
aatggtcattc catatgaaac tgagatcaact gttttgttag agaatcctca gattgagttt 120
ggatttttga gaggagagtg ttcatggaa atgagtgatt catatgtgtg ggttgagaca 180
gagtcgcagt taaaggaact tgcaaaaaata ttagcaaaag aacaagtttt tgccgttgac 240
actgagcagc atagtttgcg gtcgtttctt ggtttcactg ctctaattca gatttctaca 300
catgaggaag acttttttgtt ggacacaatt gcgttacatg atgtaatgag tattttcg 360
cctgtttctt ctgatcctaa tatttgcataag gtgtttcactg gggctgacaa cgatgttac 420
tggcttcataa gagacttcca tatataatgtt gttaatatgtt ttgataactgc caaggcatgt 480
gaagtgttgtt caaagcctca acgatcaactg gcataacttac ttgagacagt atgtggagtg 540
gctactaaca aattgctgca gcgtgaagat tggagacagc gtcctctgtc cgaagagatg 600
gtgcgatatg cttagaacaga tgcacactat ctgctttata ttgcagatag ttgcacaact 660
gaactcaaac aattagccac tggtaggcat ctttgcatac gagaaacatt ttag 714

<210> 6

<211> 237

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met Asn Leu His Phe Asp Phe Trp Cys Phe Ile Phe Glu Thr Asn Ala
1 5 10 15

Glu Lys Pro Ser Asn Gly His Pro Tyr Glu Thr Glu Ile Thr Val Leu
20 25 30

Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
35 40 45

Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
50 55 60

Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
65 70 75 80

Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
85 90 95

Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
100 105 110

His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
115 120 125

Cys Lys Val Phe His Gly Ala Asp Asn Asp Val Ile Trp Leu Gln Arg
130 135 140

Asp Phe His Ile Tyr Val Val Asn Met Phe Asp Thr Ala Lys Ala Cys
145 150 155 160

Glu Val Leu Ser Lys Pro Gln Arg Ser Leu Ala Tyr Leu Leu Glu Thr
165 170 175

Val Cys Gly Val Ala Thr Asn Lys Leu Leu Gln Arg Glu Asp Trp Arg
180 185 190

Gln Arg Pro Leu Ser Glu Glu Met Val Arg Tyr Ala Arg Thr Asp Ala
195 200 205

His Tyr Leu Leu Tyr Ile Ala Asp Ser Leu Thr Thr Glu Leu Lys Gln
210 215 220

Leu Ala Thr Gly Arg His Leu Cys Tyr Gly Glu Thr Phe
225 230 235

<210> 7
<211> 849
<212> DNA
<213> Arabidopsis thaliana

<400> 7
atgcagattg cattctctaa tgcaatatac ttgggttcatg tcacgaaagg tggagagg 60
attatgaaag cgtgttaagcc tgcaactcgag tctaattaca tcacgaaagt tattcacgt 120
tgcaagcgtg acagtggaggc tctatacttc cagtttggga taagattgca caatgttgc 180
gacactcaga ttgcttattc tctgattgaa gaacaagaag ggccggaggag acctctagat 240
gattacatat cggttgcattc actccttgct gatccacgtt actcggttat atcctatgaa 300
gagaaagaag aagttcgagt tctcatgcgc caggacccaa agtttggac atacaggcct 360
atgactgagc tcatgatccg cgcaactgtt gatgatgtcc gcttccttct gtatcttat 420
cacaaaatga tggaaagct aaatcagcgg tcactatggc atcttgcaatg tcgtgggt 480
ttgtactgtc ggtgtctctg ctgcattcatgat gatgctgattt ttgctgattt gccaaccgtt 540
cctccaaattc cagtttgcct cgttaaggcgt gtatatgtc tagagacaaa gaaaaaaaaga 600
cgggtgacat tagcttcgtat tgggttactg attgttagttt gactttttaaat tggcagat 660
aacctgaagt cagaagatca atgtcttgc gaaagagatcc tgcgtgttgc tgcgtttcca 720
ccaggaaaga tgggacgtgt gatttgcagg aaaggagcat cgatcctcgc cattaaggaa 780
gcttgcaacg cggaaattct aatttggagg gcaaagggtc cacctgataa gtttagtctt 840
attccatag 849

<210> 8
<211> 282
<212> PRT
<213> Arabidopsis thaliana

<400> 8
Met Gln Ile Ala Phe Ser Asn Ala Ile Tyr Leu Val Asp Val Ile Glu
1 5 10 15

Gly Gly Glu Val Ile Met Lys Ala Cys Lys Pro Ala Leu Glu Ser Asn
20 25 30

Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu
35 40 45

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
50 55 60

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
65 70 75 80

Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
85 90 95

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
 100 105 110
 Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
 115 120 125
 Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
 130 135 140
 Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
 145 150 155 160
 Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
 165 170 175
 Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
 180 185 190
 Ala Val Glu Thr Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
 195 200 205
 Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
 210 215 220
 Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
 225 230 235 240
 Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
 245 250 255
 Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
 260 265 270
 Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
 275 280

<210> 9
 <211> 720
 <212> DNA
 <213> *Arabidopsis thaliana*

<400> 9
 atggcttagga tcagaagaag aatccaaaag cgccatatcc acgaaaaccg ctacatcgat 60
 ttctttggag aacgttgat cgtcacggtc actcatacta cctcaaccat cgcgcgttgg 120
 attcatagca tccgttctt cagccgtctt cgctcctcac accctctcggt tgttggactc 180
 gacgtccaaat ggacaccggg tggttccgat cctccaccgg atattctcca actatgtgtt 240
 ggttaaccgct gtctcatcat ccagttgtct cactgtaaac gcattcctgaa ggtccttcga 300
 agtttcttgg aagatgagac aatcaactttt gtcggcgtct ggaacagcca agaccaggc 360
 aagctcgaaa gattccgcca tcagttggag atatggagac ttcttagacat aaggcactat 420
 ctgcctacga ggctcctcaa tagttcggtt gagaagattt tagaggagtg tttggggtagc 480
 aaggaggatgtt gggatgtt atgagtaatt ggggtgctcg tagcctttcc 540
 catgatcaga ttgttcagggc gtcagatgtat gtctatgttt gctgcaagct cgggtttaag 600
 gaatgtatctt gggatgtt aaagaacgtt tctggaaaga gagctcgaat 660
 gttaaggaac atatctggaa agagagctcg aaactttatt ttgttgggtt atgtttctga 720

<210> 10
<211> 239
<212> PRT
<213> Arabidopsis thaliana

<400> 10
Met Ala Arg Ile Arg Arg Arg Ile Gln Lys Arg His Ile His Glu Asn
1 5 10 15

Arg Tyr Ile Asp Phe Phe Gly Glu Arg Leu Ile Val Thr Val Thr His
20 25 30

Thr Thr Ser Thr Ile Arg Arg Trp Ile His Ser Ile Arg Phe Phe Ser
35 40 45

Arg Leu Arg Ser Ser His Pro Leu Val Val Gly Leu Asp Val Gln Trp
50 55 60

Thr Pro Gly Gly Ser Asp Pro Pro Asp Ile Leu Gln Leu Cys Val
65 70 75 80

Gly Asn Arg Cys Leu Ile Ile Gln Leu Ser His Cys Lys Arg Ile Pro
85 90 95

Glu Val Leu Arg Ser Phe Leu Glu Asp Glu Thr Ile Thr Phe Val Gly
100 105 110

Val Trp Asn Ser Gln Asp Gln Gly Lys Leu Glu Arg Phe Arg His Gln
115 120 125

Leu Glu Ile Trp Arg Leu Leu Asp Ile Arg His Tyr Leu Pro Thr Arg
130 135 140

Leu Leu Asn Ser Ser Phe Glu Lys Ile Val Glu Glu Cys Leu Gly Tyr
145 150 155 160

Lys Gly Val Arg Lys Asp Lys Glu Ile Cys Met Ser Asn Trp Gly Ala
165 170 175

Arg Ser Leu Ser His Asp Gln Ile Val Gln Ala Ser Asp Asp Val Tyr
180 185 190

Val Cys Cys Lys Leu Gly Val Lys Glu Cys Ile Trp Lys Glu Arg Ser
195 200 205

Asn Val Lys Glu Arg Ile Trp Lys Glu Ser Ser Asn Val Lys Glu His
210 215 220

Ile Trp Lys Glu Ser Ser Lys Leu Tyr Phe Val Gly Val Cys Phe
225 230 235

<210> 11
<211> 654
<212> DNA
<213> Arabidopsis thaliana

<400> 11

atgaagagag gtatcaaaca tctatgtttc aatggcttca cgggctactc atcacttcat 60
 catcattatc atgaacaccca cgctgacttc tttggagaac gtttgatcgt cacagtca 120
 catactccct cagtgatacg tcgatggatc cacagtatcc gcttcgtca gcttcgc 180
 ttatcacacc ctctagttgt cgacttggc gttcaatgga caccccggtgg ttccgatcct 240
 ccaccggata ttctccaaact atgtgttggt actcgctgtc tcatcattca gttgtctcac 300
 tgtaagtacg tccccgacgt ccttagaagt ttcttggaaatcagacaat cactttgtc 360
 ggcgtatgga acagccaaaga caaggacaag ctcgagagat tccaccatca gttggatatc 420
 tggagacttg tccacataag gcactatctc catccgttgc tcttgagtag ctcgtttgag 480
 acgattgtga aggtgtattt ggggcatgaa ggagtgacga aagataagga gttatgtatg 540
 agtaattggg gtgctcgtag cctctctcat gatcagatag tacaagcgtc acatgatgtc 600
 tatgtttgct gcaagctcgg tgttaaggaa cgtctctgga aaatgggagc ttaa 654

<210> 12
 <211> 217
 <212> PRT
 <213> Arabidopsis thaliana

<400> 12

Met	Lys	Arg	Gly	Ile	Lys	His	Leu	Cys	Phe	Asn	Gly	Phe	Thr	Gly	Tyr
1															15
Ser	Ser	Leu	His	His	His	Tyr	His	Glu	His	His	Val	Asp	Phe	Phe	Gly
								20			25				30
Glu	Arg	Leu	Ile	Val	Thr	Val	Thr	His	Thr	Pro	Ser	Val	Ile	Arg	Arg
								35			40				45
Trp	Ile	His	Ser	Ile	Arg	Phe	Val	Ser	Arg	Leu	Arg	Leu	Ser	His	Pro
								50			55				60
Leu	Val	Val	Gly	Leu	Gly	Val	Gln	Trp	Thr	Pro	Arg	Gly	Ser	Asp	Pro
							65			70		75			80
Pro	Pro	Asp	Ile	Leu	Gln	Leu	Cys	Val	Gly	Thr	Arg	Cys	Leu	Ile	Ile
								85			90				95
Gln	Leu	Ser	His	Cys	Lys	Tyr	Val	Pro	Asp	Val	Leu	Arg	Ser	Phe	Leu
								100			105				110
Glu	Asp	Gln	Thr	Ile	Thr	Phe	Val	Gly	Val	Trp	Asn	Ser	Gln	Asp	Lys
								115			120				125
Asp	Lys	Leu	Glu	Arg	Phe	His	His	Gln	Leu	Asp	Ile	Trp	Arg	Leu	Val
								130			135				140
His	Ile	Arg	His	Tyr	Leu	His	Pro	Leu	Leu	Leu	Ser	Ser	Ser	Phe	Glu
								145			150				160
Thr	Ile	Val	Lys	Val	Tyr	Leu	Gly	His	Glu	Gly	Val	Thr	Lys	Asp	Lys
								165			170				175
Glu	Leu	Cys	Met	Ser	Asn	Trp	Gly	Ala	Arg	Ser	Leu	Ser	His	Asp	Gln
								180			185				190
Ile	Val	Gln	Ala	Ser	His	Asp	Val	Tyr	Val	Cys	Cys	Lys	Leu	Gly	Val

195	200	205
Lys Glu Arg Leu Trp Lys Met Gly Ala		
210	215	
<210> 13		
<211> 261		
<212> DNA		
<213> <i>Arabidopsis thaliana</i>		
<400> 13		
atgatcaagt cgatcgagag ctttattgct cgttatgttt tccaagctac attatacaca 60		
atctggcg aacgaaatgg cagaaggcat ggagagagag aggccgaacc agccgcttt 120		
ctaataaaat tgattgataa gcaagccatc tttcctcaat cagagcaact gatgatctac 180		
gctatgacaa gaggctccaa atctggtttgcatcgagtgg ttgaaatcaa accatctata 240		
gttcatgtgt ttaaccttta a 261		
<210> 14		
<211> 86		
<212> PRT		
<213> <i>Arabidopsis thaliana</i>		
<400> 14		
Met Ile Lys Ser Ile Glu Ser Phe Ile Ala Arg Tyr Val Phe Gln Ala		
1	5	10
		15
Thr Leu Tyr Thr Ile Trp Cys Glu Arg Asn Gly Arg Arg His Gly Glu		
20	25	30
Arg Glu Ala Glu Pro Ala Ala Leu Leu Ile Lys Leu Ile Asp Lys Gln		
35	40	45
Ala Ile Phe Pro Gln Ser Glu Gln Leu Met Ile Tyr Ala Met Thr Arg		
50	55	60
Ala Ser Lys Ser Gly Leu His Arg Val Val Glu Ile Lys Pro Ser Ile		
65	70	75
		80
Val His Val Phe Asn Leu		
	85	
<210> 15		
<211> 2733		
<212> DNA		
<213> <i>C. elegans</i>		
<400> 15		
atgaaagaag aaccgtacaa aagaaagcta acgaaagccg agaaaaaggc aaaatatacg 60		
acagactacg ccgaaccgtt gaagtacgcg cggaaagtcc tgaaagcaat tatgaatgg 120		
cccgagtctg agcgggagag aaaagttcga gccaaaaatc gagaattttt caacgaggac 180		
tatagatcg gagtcaacat ctacggatg gctgtggata tgatgaaagc gatgccggat 240		
agaggaaaaa catcgggaca aagttggcg gtttggatc tggaggatt tggagttgg 300		
ttaaaagagt cgggacagga gacggagctc agacagaaat atctgactgg aactattcaa 360		
ataaacgcct tagatgtgtcacaattgga caaaagcagc ttctcagtga aatcttcgtat 420		

atcaccaaag agaaattcac tgaggacatt acacagttgc tagatgctgc catcaagaaa 480
caagacttct ccgttgcgtc agatatggct attcagtaca atcttctacg ggatcatcat 540
ttcgaacatc ttgttcttcc attaatgcta tctggcaaag atcaaacggc ttataaattg 600
ataagtaaca atgagaggat gcaacagcag cttgttagt ttttgatcg aatggttgga 660
atctcagtgg ttgcgttga agagatgctg aaaccctaca agggaaaccaa aattatgacg 720
attcctatgg agaaattgac gggaaaaacg ttggacaaac tcatttcgac gattatcaac 780
aaaaatactc acgaatacaa cttctccagg gaattgtcga agttcgccaa aaaccoactca 840
cagaatggga atctgaaggc attgaagttt aatatcagtg aacgatacga gaaggaaaa 900
tccgatgaca actatttca gcatatggtt gaaacttta ccaaagccga agatgtcgt 960
gaacctattt tggttactt gtggagctca aatgacaccg agaaacaaat agatgccatc 1020
tgctttgcta tctacttagg aatcgctagt tccagcagct atcaactgacg gaatgttatg 1080
aggacttct ttgcacaacc tgattcgaag ctcagagaag caaaagaact tctagtgaga 1140
agaaaaacac tgcaagttcc tctaaatggc gaacaattat tcgtatttga gaatgagcga 1200
agaactcaaa tccacatggt gaaaactgaa tctgagatga attacttatg ttccgagatc 1260
aaatcactaa gcgacgagcc agcacctgtt tacgttggat tcgattctga gtggaaacccg 1320
tcgaatctta cagctgttca tgactcgaaa attgctatca tacaatttgcgatc 1380
tgtgtatggc ttgtggattt cgtagaatta gaaaaggcaaa atatggcaga tgactggatg 1440
caaaagttcg catctcgatt gttcggagat tctcctgtaa aagtcgtagg atttgcata 1500
aggaacgatc tggatgcaat ggctacaatc ccagcaactga agtcatccat gaagatagaa 1560
gataccaaaa atgcattcga tctgaagcga ttagcagaga atggttgcga tatcgacatg 1620
gaaattttag agctgccaaa gaagacttcc aaattggcag atttgacaca ttatctactg 1680
ggattggagc tcgacaaaac tgaacaatgc agtaactggc aatgtcgatc tctgcgaaaa 1740
aaacaaattt tgtagcgcgc attggacgca gttgtcgatc ttggaaacattt caagaaaaatc 1800
ttgtcgattt tagaggagaa aaacaaggac gcagatatcg agaagatttgcgatc 1860
aatgtatgg ctccgaaaaa agacaaagga cacaatcgt accgcaagct gaaaactatt 1920
ccatggctt agctctacga tatcttgcga agccatcgta atcctacgag atcaccacag 1980
cgaccacacg acattaaagt tattgttgcgatc acaatgctga ttggatttgcgatc 2040
aggagagttt gaattgtatgt tattttccaa aaagacgtga gcgacttccg aaagtacactg 2100
aagaaattt aacgagttgg cggcggatcatc ttagtgcata taatcacatg gccatcgaaa 2160
agttacgaaat ctttgcgatc ggattatgtt aattatacaa ttgcaattcc ggaactcaat 2220
aacatgtctc ccgttagatca gcttatttgcgatc ttgttgcgatc ttgttgcgatc 2280
ccggaagacg tatattcccg atgcactgaa tgcaatttgcgatc ggcttcaat taaattcccc 2340
ggaccagttt tacatttctt gcaccaatac tttgttgcgatc atgtgcggatc ttgttgcgatc 2400
gctgatgtt gcaatttcc acttggaaatggatc ttgttgcgatc ttgttgcgatc 2460
gacgactacg acggataaa atgttgcgatc ttgttgcgatc ttgttgcgatc 2520
gtggcaacttgg tttccacagg atgcctacat attacgcgcgaaatgcact tcacaccaat 2580
ctggccagatg gaatttgcgatc ttgttgcgatc ttgttgcgatc ttgttgcgatc 2640
aatctcgttgcgatc ttgttgcgatc ttgttgcgatc ttgttgcgatc ttgttgcgatc 2700
caagcgtcgagatc ttgttgcgatc ttgttgcgatc ttgttgcgatc ttgttgcgatc 2733

<210> 16
<211> 910
<212> PRT
<213> C. elegans

<400> 16
Met Glu Glu Glu Pro Tyr Lys Arg Lys Leu Thr Lys Ala Glu Lys Lys
1 5 10 15

Ala Lys Tyr Arg Thr Asp Tyr Ala Glu Pro Leu Lys Ser Arg Arg Glu
20 25 30

Val Leu Lys Ala Ile Met Asn Gly Pro Glu Ser Glu Arg Glu Arg Lys
35 40 45

Val Arg Ala Lys Asn Arg Glu Phe Phe Asn Glu Asp Tyr Arg Ser Gly

50	55	60																																																																																																																					
Val Asn Ile Tyr Gly Met Ala Val Asp Met Met Lys Ala Met Pro Asp																																																																																																																							
65	70	75	80			Arg Gly Lys Thr Ser Gly Gln Ser Leu Ala Val Trp Tyr Leu Glu Asp			85	90	95	Phe Gly Val Trp Leu Lys Glu Ser Gly Gln Glu Thr Glu Leu Arg Gln			100	105	110	Lys Tyr Leu Thr Gly Thr Ile Gln Ile Asn Ala Leu Asp Val Cys Thr			115	120	125	Ile Gly Gln Lys Gln Leu Leu Ser Glu Ile Phe Asp Ile Thr Lys Glu			130	135	140	Lys Phe Thr Glu Asp Ile Thr Gln Leu Leu Asp Ala Ala Ile Lys Lys			145	150	155	160			Gln Asp Phe Ser Val Ala Ala Asp Met Ala Ile Gln Tyr Asn Leu Leu			165	170	175	Arg Asp His His Phe Glu His Leu Val Leu Pro Leu Met Leu Ser Gly			180	185	190	Lys Asp Gln Thr Ala Tyr Lys Leu Ile Ser Asn Asn Glu Arg Met Gln			195	200	205	Gln Gln Leu Val Glu Phe Phe Asp Arg Met Val Gly Ile Ser Val Val			210	215	220	Ala Val Glu Glu Met Leu Lys Pro Tyr Lys Glu Thr Lys Ile Met Thr			225	230	235	240			Ile Pro Met Glu Lys Leu Thr Gly Lys Thr Leu Asp Lys Leu Ile Ser			245	250	255	Thr Ile Ile Asn Lys Asn Thr His Glu Tyr Asn Phe Ser Arg Glu Leu			260	265	270	Ser Lys Phe Ala Lys Asn His Ser Gln Asn Gly Asn Leu Lys Ala Leu			275	280	285	Lys Phe Asn Ile Ser Glu Arg Tyr Glu Lys Gly Lys Ser Asp Asp Asn			290	295	300	Tyr Phe Gln His Met Val Glu Thr Phe Thr Lys Ala Glu Asp Val Arg			305	310	315	320			Glu Pro Ile Leu Phe Tyr Leu Trp Ser Ser Asn Asp Thr Glu Lys Gln			325	330	335	Ile Asp Ala Ile Cys Phe Ala Ile Tyr Leu Gly Ile Ala Ser Ser Ser			340	345	350	Ser Tyr Gln Leu Pro Asn Val Met Arg Asp Phe Phe Arg Gln Pro Asp		
80																																																																																																																							
Arg Gly Lys Thr Ser Gly Gln Ser Leu Ala Val Trp Tyr Leu Glu Asp																																																																																																																							
85	90	95																																																																																																																					
Phe Gly Val Trp Leu Lys Glu Ser Gly Gln Glu Thr Glu Leu Arg Gln																																																																																																																							
100	105	110																																																																																																																					
Lys Tyr Leu Thr Gly Thr Ile Gln Ile Asn Ala Leu Asp Val Cys Thr																																																																																																																							
115	120	125																																																																																																																					
Ile Gly Gln Lys Gln Leu Leu Ser Glu Ile Phe Asp Ile Thr Lys Glu																																																																																																																							
130	135	140																																																																																																																					
Lys Phe Thr Glu Asp Ile Thr Gln Leu Leu Asp Ala Ala Ile Lys Lys																																																																																																																							
145	150	155	160			Gln Asp Phe Ser Val Ala Ala Asp Met Ala Ile Gln Tyr Asn Leu Leu			165	170	175	Arg Asp His His Phe Glu His Leu Val Leu Pro Leu Met Leu Ser Gly			180	185	190	Lys Asp Gln Thr Ala Tyr Lys Leu Ile Ser Asn Asn Glu Arg Met Gln			195	200	205	Gln Gln Leu Val Glu Phe Phe Asp Arg Met Val Gly Ile Ser Val Val			210	215	220	Ala Val Glu Glu Met Leu Lys Pro Tyr Lys Glu Thr Lys Ile Met Thr			225	230	235	240			Ile Pro Met Glu Lys Leu Thr Gly Lys Thr Leu Asp Lys Leu Ile Ser			245	250	255	Thr Ile Ile Asn Lys Asn Thr His Glu Tyr Asn Phe Ser Arg Glu Leu			260	265	270	Ser Lys Phe Ala Lys Asn His Ser Gln Asn Gly Asn Leu Lys Ala Leu			275	280	285	Lys Phe Asn Ile Ser Glu Arg Tyr Glu Lys Gly Lys Ser Asp Asp Asn			290	295	300	Tyr Phe Gln His Met Val Glu Thr Phe Thr Lys Ala Glu Asp Val Arg			305	310	315	320			Glu Pro Ile Leu Phe Tyr Leu Trp Ser Ser Asn Asp Thr Glu Lys Gln			325	330	335	Ile Asp Ala Ile Cys Phe Ala Ile Tyr Leu Gly Ile Ala Ser Ser Ser			340	345	350	Ser Tyr Gln Leu Pro Asn Val Met Arg Asp Phe Phe Arg Gln Pro Asp																																			
160																																																																																																																							
Gln Asp Phe Ser Val Ala Ala Asp Met Ala Ile Gln Tyr Asn Leu Leu																																																																																																																							
165	170	175																																																																																																																					
Arg Asp His His Phe Glu His Leu Val Leu Pro Leu Met Leu Ser Gly																																																																																																																							
180	185	190																																																																																																																					
Lys Asp Gln Thr Ala Tyr Lys Leu Ile Ser Asn Asn Glu Arg Met Gln																																																																																																																							
195	200	205																																																																																																																					
Gln Gln Leu Val Glu Phe Phe Asp Arg Met Val Gly Ile Ser Val Val																																																																																																																							
210	215	220																																																																																																																					
Ala Val Glu Glu Met Leu Lys Pro Tyr Lys Glu Thr Lys Ile Met Thr																																																																																																																							
225	230	235	240			Ile Pro Met Glu Lys Leu Thr Gly Lys Thr Leu Asp Lys Leu Ile Ser			245	250	255	Thr Ile Ile Asn Lys Asn Thr His Glu Tyr Asn Phe Ser Arg Glu Leu			260	265	270	Ser Lys Phe Ala Lys Asn His Ser Gln Asn Gly Asn Leu Lys Ala Leu			275	280	285	Lys Phe Asn Ile Ser Glu Arg Tyr Glu Lys Gly Lys Ser Asp Asp Asn			290	295	300	Tyr Phe Gln His Met Val Glu Thr Phe Thr Lys Ala Glu Asp Val Arg			305	310	315	320			Glu Pro Ile Leu Phe Tyr Leu Trp Ser Ser Asn Asp Thr Glu Lys Gln			325	330	335	Ile Asp Ala Ile Cys Phe Ala Ile Tyr Leu Gly Ile Ala Ser Ser Ser			340	345	350	Ser Tyr Gln Leu Pro Asn Val Met Arg Asp Phe Phe Arg Gln Pro Asp																																																																				
240																																																																																																																							
Ile Pro Met Glu Lys Leu Thr Gly Lys Thr Leu Asp Lys Leu Ile Ser																																																																																																																							
245	250	255																																																																																																																					
Thr Ile Ile Asn Lys Asn Thr His Glu Tyr Asn Phe Ser Arg Glu Leu																																																																																																																							
260	265	270																																																																																																																					
Ser Lys Phe Ala Lys Asn His Ser Gln Asn Gly Asn Leu Lys Ala Leu																																																																																																																							
275	280	285																																																																																																																					
Lys Phe Asn Ile Ser Glu Arg Tyr Glu Lys Gly Lys Ser Asp Asp Asn																																																																																																																							
290	295	300																																																																																																																					
Tyr Phe Gln His Met Val Glu Thr Phe Thr Lys Ala Glu Asp Val Arg																																																																																																																							
305	310	315	320			Glu Pro Ile Leu Phe Tyr Leu Trp Ser Ser Asn Asp Thr Glu Lys Gln			325	330	335	Ile Asp Ala Ile Cys Phe Ala Ile Tyr Leu Gly Ile Ala Ser Ser Ser			340	345	350	Ser Tyr Gln Leu Pro Asn Val Met Arg Asp Phe Phe Arg Gln Pro Asp																																																																																																					
320																																																																																																																							
Glu Pro Ile Leu Phe Tyr Leu Trp Ser Ser Asn Asp Thr Glu Lys Gln																																																																																																																							
325	330	335																																																																																																																					
Ile Asp Ala Ile Cys Phe Ala Ile Tyr Leu Gly Ile Ala Ser Ser Ser																																																																																																																							
340	345	350																																																																																																																					
Ser Tyr Gln Leu Pro Asn Val Met Arg Asp Phe Phe Arg Gln Pro Asp																																																																																																																							

355	360	365
Ser Lys Leu Arg Glu Ala Lys Glu Leu Leu Val Arg Arg Lys Thr Leu		
370	375	380
Gln Val Pro Leu Asn Gly Glu Gln Leu Phe Val Phe Glu Asn Glu Arg		
385	390	395
Arg Thr Gln Ile His Met Val Lys Thr Glu Ser Glu Met Asn Tyr Leu		
405	410	415
Cys Ser Glu Ile Lys Ser Leu Ser Asp Glu Pro Ala Pro Val Tyr Val		
420	425	430
Gly Phe Asp Ser Glu Trp Lys Pro Ser Asn Leu Thr Ala Val His Asp		
435	440	445
Ser Lys Ile Ala Ile Ile Gln Leu Phe Phe Lys Asn Cys Val Trp Leu		
450	455	460
Val Asp Cys Val Glu Leu Glu Lys Ala Asn Met Ala Asp Asp Trp Trp		
465	470	475
480		
Gln Lys Phe Ala Ser Arg Leu Phe Gly Asp Ser Pro Val Lys Val Val		
485	490	495
Gly Phe Asp Met Arg Asn Asp Leu Asp Ala Met Ala Thr Ile Pro Ala		
500	505	510
Leu Lys Ser Ser Met Lys Ile Glu Asp Thr Lys Asn Ala Phe Asp Leu		
515	520	525
Lys Arg Leu Ala Glu Asn Val Cys Asp Ile Asp Met Glu Ile Leu Glu		
530	535	540
Leu Pro Lys Lys Thr Phe Lys Leu Ala Asp Leu Thr His Tyr Leu Leu		
545	550	555
560		
Gly Leu Glu Leu Asp Lys Thr Glu Gln Cys Ser Asn Trp Gln Cys Arg		
565	570	575
Pro Leu Arg Lys Lys Gln Ile Val Tyr Ala Ala Leu Asp Ala Val Val		
580	585	590
Val Val Glu Thr Phe Lys Lys Ile Leu Ser Ile Val Glu Glu Lys Asn		
595	600	605
Lys Asp Ala Asp Ile Glu Lys Ile Val Arg Glu Ser Asn Val Met Ala		
610	615	620
Pro Lys Lys Asp Lys Gly His Lys Ser Tyr Arg Lys Leu Lys Thr Ile		
625	630	635
640		
Pro Trp Leu Glu Leu Tyr Asp Ile Leu Arg Ser His Arg Asn Pro Thr		
645	650	655
Arg Ser Pro Gln Arg Pro His Asp Ile Lys Val Ile Val Asp Thr Met		

660	665	670
Leu Ile Gly Phe Gly Lys Asn Leu Arg Arg Val Gly Ile Asp Val Ile		
675	680	685
Leu Pro Lys Asp Val Ser Asp Phe Arg Lys Tyr Leu Lys Glu Ile Glu		
690	695	700
Arg Val Gly Gly Glu His Leu Arg His Ile Ile Thr Val Pro Ser Lys		
705	710	715
Ser Tyr Glu Ala Leu Lys Met Asp Tyr Asp Asn Tyr Thr Ile Ala Ile		
725	730	735
Pro Glu Leu Asn Asn Met Ser Pro Val Asp Gln Leu Ile Glu Phe Phe		
740	745	750
Asp Leu Phe Asn Val Asp Ile Arg Pro Glu Asp Val Tyr Pro Arg Cys		
755	760	765
Thr Glu Cys Asn Ser Arg Leu Gln Ile Lys Phe Pro Gly Pro Val Leu		
770	775	780
His Phe Leu His Gln Tyr Cys Val Ile His Val Gln Asn Val Tyr Arg		
785	790	795
Ala Asp Met Ser Glu Phe Pro Leu Glu Glu Trp Trp Asn Arg Met Leu		
805	810	815
His Ile Asn Pro Asp Asp Tyr Asp Gly Val Lys Val Glu Met Ser Arg		
820	825	830
Pro Ser Pro Thr Ser Lys Trp Ile Val Ala Thr Val Pro Thr Gly Cys		
835	840	845
Leu His Ile Thr Arg Gln Thr Ala Leu His Thr Asn Leu Pro Asp Gly		
850	855	860
Ile Glu Val Arg Ile His Lys Val Pro Asp Asp Glu Phe Lys Arg Arg		
865	870	875
880		
Asn Leu Ser Phe Tyr Val Cys Gly Glu Cys Gly Thr Val Ala Cys Asp		
885	890	895
Gly Arg Gly Asn Gln Ala Ser Glu Ser Thr Ser Gln Glu Cys		
900	905	910

<210> 17
 <211> 4299
 <212> DNA
 <213> Homo sapiens

<400> 17
 atagagtggaa aaaaattgga aacaactgca cagcagcgga aatgtcctga atggatgaat 60
 gtgcagaata aaagatgtgc tgtagaagaa agaaaggcat gtgttcggaa gagtgtttt 120
 gaagatgacc tcccctctt agaattcact ggatccattg tgtatagttt cgatgctagt 180

gattgctctt tcctgtcaga agatattagc atgagtctat cagatgggga tgtggtggga 240
 tttgacatgg agtggccacc attatacaat agaggaaac ttggcaaagt tgcactaatt 300
 cagttgtgt tttctgagag caaatgtac ttgtccacg tttcttccat gtcagtttt 360
 cccaggat taaaatgtt gcttaaaat aaagcagtt aaaaggcagg tgttagaatt 420
 gaaggagatc agtggaaact tctacgtac tttgatatac aattgaagaa ttttggag 480
 ttgacagatg ttgccaataa aaagctgaaa tgtacagaga cctggagcc taacagtctg 540
 gttaaacacc tcttaggtaa acagctcctg aaagacaagt ctatccgctg tagcaattgg 600
 agtaaatttc ctctcactga ggaccagaaa ctgtatgcg ccaactgatgc ttatgcttgt 660
 tttattattt accgaaattt agagatttg gatgatactg tgcaaagggt tgctataat 720
 aaagaggaag aaatcctact taggcacatg aacaaacagt tgacttcaat ctctgaggaa 780
 gtgatggatc tggctaagca tcttcctcat gcttcagta aattggaaaa cccacggagg 840
 gtttctatct tactaaagga tatttcagaa aatctatatt cactgaggag gatgataatt 900
 gggctacta acattgagac tgaactgagg cccagcaata attaaactt attatcctt 960
 gaagattcaa ctactgggg agtacaacag aaacaatta gagaacatga agtttaatt 1020
 cacgttgaag atgaaacatg ggacccaaca cttgatcatt tagctaaaca tgatggagaa 1080
 gatgtactt gaaataaagt ggaacgaaaa gaagatggat ttgaagatgg agtagaaagac 1140
 aacaattga aagagaatat gggaaagagct tggttgcgt cgtagatatacagaacat 1200
 gaactccaaa ttttggaca gcagtctcag gaagaatatac tttagtgcata tgcttataaa 1260
 tctactgagc atttatctcc caatgataat gaaaacgata cgtcctatgt aattgagagt 1320
 gatgaagatt tagaaatgga gatgcttaag catttatctc ccaatgataa tgaaaacgat 1380
 acgtcctatg taattgagag ttagaaatgg agatgcttaa gtctttagaa 1440
 aacctcaata gtggcacggt agaaccact cattctaaat gcttaaaaat gggaaagaaat 1500
 ctgggtcttc ctactaaaga agaagaagaa gatgatgaaa atgaagctaa tgaaggggaa 1560
 gaagatgatg ataaggactt ttttggcca gcacccaaatg aagagcaagt tacttgctc 1620
 aagatgtact ttggccattc cagttttaaa ccagttcagt gggaaagtgtat tcattcaga 1680
 ttagaagaaa gaagagataa tggctgtc atggcaactg gatatggaaa gagtttgc 1740
 ttccagttatc cacctgttta tggtagcaag attggcctt ttagtctcc ctttatttct 1800
 ctgatggaa accaagtgc acagcttaaa atgtccaaaca tcccagctt cttccttgg 1860
 tcagcacagt cagaaaatgt tctaacagat attaaattag gtaaataccg gattgtatac 1920
 gtaactccag aatactgttc agtaacatg ggcctgctcc agcaacttga ggctgatatt 1980
 ggtatcacgc tcattgtgt ggttagggct cactgtattt ctgagtggg gcatgatttt 2040
 agggattcat tcaggaagtt gggctcccta aagacacac tgccaaatggt tccaaatcg 2100
 gcacttactg ctactgcaag ttcttcaatc cgggaagaca ttgtacgtt cttaaatctg 2160
 agaaatcctc agatcacctg tactggttt gatcgaccaaa acctgtattt agaagttagg 2220
 cgaaaaacag ggaatatacct tcaggatctg cagccattt ttgtcaaaac aagttcccac 2280
 tggaaattt aaggcacaac aatcatctac tggcttctta gaaaaatgac acaacaagtt 2340
 acaggtgaac ttagaaact taatctatcc tggaaacat accatgcggg catgatgttt 2400
 agcacaagga aagacattca tcatacgat tggaaatggt gtaagagatg aaattcagtg tgcatacgat 2460
 accatagctt ttggaaatggg cattaataaa gctgacattc gccaagtcat tcattacgg 2520
 gctcctaagg acatggaaatc atattatcg gagattggta gagctggcg tgatggactt 2580
 caaagttctt gtcacgtcct ctggcgtcct gcagacatta actttaatag gcaccttctt 2640
 actgagatac gtaatgagaa gttcgatatacataaattaa agatgatggc aaagatggaa 2700
 aaatatcttc attctagcag atgtaggaga caaatcatct tggctcattt tgaggacaaa 2760
 caagtacaaa aagcctccctt gggaaattatg ggaactgaaa aatgctgtga taattgcagg 2820
 tccagattgg atcattgtca ttccatggat gactcagagg atacatcctg ggactttgg 2880
 ccacaagcat ttaagcttt gttctgtgt gacatcttgc gcgaaaaatt tggaattggg 2940
 cttccaaattt tatttcctcg agatctaat ttcacgtc ttgcccgtca atatcgagg 3000
 cacagttat ttggcactgg caaggatcaa acagagatgg ggtggaaaggc ttttccgt 3060
 cagctgatca ctggggatt ctggtagaa gtttctcggt ataaacaaatt tatgaagatt 3120
 tggccctta cgaaaaagg tagaaattgg cttcataaag ctaatacaga atctcagagc 3180
 ctcatccttc aagctaatacaga aagattgtgt ccaaaagaatg ttcttctgccc tagttcgaaa 3240
 actgtatctt cgggcaccaa agacattgt tataatcaag taccagttga attaagtaca 3300
 gagaagaagt ctaacttggaa gaagttatac tcttataaact catgtataa gatttcttct 3360
 gggagtaaca tttctaaaaa aagtatcatg gtacagtccac cagaaaaagc ttacagttcc 3420
 tcacagcctg ttatttcggc acaagagcag gagactcaga ttgtgttata tggcaaattg 3480
 gtagaagcta ggcagaaaca tgccataaaa atggatgttc cccagctat tctggcaaca 3540
 aacaagatac tggtgatatac ggcaccaatg agaccaacta cggttggaaaa cgtaaaaagg 3600

attgatggc tttctgaagg caaagctgcc atgtggccc ctctgttgg agtcatcaaa 3660
 catttctgcc aaacaaatag tggtcagaca gacctcttt caagtacaaa acctcaagaa 3720
 gaacagaaga cgagtctggt agcaaaaaat aaaatatgca cactttcaca gtctatggcc 3780
 atcacatact ctttattcca agaaaagaag atgccttga agagcatagc tgagagcagg 3840
 attctgcctc tcatgacaat tggcatgcac ttatccaag cggtgaaagc tggctgcccc 3900
 cttgatttgg agcgagcagg cctgactcca gaggttcaga agattattgc tgatgttatac 3960
 cggaaaccctc ccgtcaactc agatatgagt aaaattagcc taatcagaat gttagttcct 4020
 gaaaacattg acacgtaccc tatccacatg gcaattgaga tccttaaaca tggtcctgac 4080
 agcggacttc aactttcatg tgatgtcaac aaaaggagat gtttcccggttctgaagag 4140
 atctgttcaa gttctaagag aagcaaggaa gaagtaggca tcaatactga gacttcatct 4200
 gcagagagaa agagacgatt acctgtgtgg tttgccaaag gaagtgatac cagcaagaaa 4260
 ttaatggaca aaacgaaaag gggaggtctt ttttagttaa 4299

<210> 18
 <211> 1432
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Ser Glu Lys Lys Leu Glu Thr Thr Ala Gln Gln Arg Lys Cys Pro
 1 5 10 15

Glu Trp Met Asn Val Gln Asn Lys Arg Cys Ala Val Glu Glu Arg Lys
 20 25 30

Ala Cys Val Arg Lys Ser Val Phe Glu Asp Asp Leu Pro Phe Leu Glu
 35 40 45

Phe Thr Gly Ser Ile Val Tyr Ser Tyr Asp Ala Ser Asp Cys Ser Phe
 50 55 60

Leu Ser Glu Asp Ile Ser Met Ser Leu Ser Asp Gly Asp Val Val Gly
 65 70 75 80

Phe Asp Met Glu Trp Pro Pro Leu Tyr Asn Arg Gly Lys Leu Gly Lys
 85 90 95

Val Ala Leu Ile Gln Leu Cys Val Ser Glu Ser Lys Cys Tyr Leu Phe
 100 105 110

His Val Ser Ser Met Ser Val Phe Pro Gln Gly Leu Lys Met Leu Leu
 115 120 125

Glu Asn Lys Ala Val Lys Lys Ala Gly Val Gly Ile Glu Gly Asp Gln
 130 135 140

Trp Lys Leu Leu Arg Asp Phe Asp Ile Lys Leu Lys Asn Phe Val Glu
 145 150 155 160

Leu Thr Asp Val Ala Asn Lys Lys Leu Lys Cys Thr Glu Thr Trp Ser
 165 170 175

Leu Asn Ser Leu Val Lys His Leu Leu Gly Lys Gln Leu Leu Lys Asp
 180 185 190

Lys Ser Ile Arg Cys Ser Asn Trp Ser Lys Phe Pro Leu Thr Glu Asp

195	200	205
Gln Lys Leu Tyr Ala Ala Thr Asp Ala Tyr Ala Gly Phe Ile Ile Tyr		
210	215	220
Arg Asn Leu Glu Ile Leu Asp Asp Thr Val Gln Arg Phe Ala Ile Asn		
225	230	235
240		
Lys Glu Glu Glu Ile Leu Leu Ser Asp Met Asn Lys Gln Leu Thr Ser		
245	250	255
Ile Ser Glu Glu Val Met Asp Leu Ala Lys His Leu Pro His Ala Phe		
260	265	270
Ser Lys Leu Glu Asn Pro Arg Arg Val Ser Ile Leu Leu Lys Asp Ile		
275	280	285
Ser Glu Asn Leu Tyr Ser Leu Arg Arg Met Ile Ile Gly Ser Thr Asn		
290	295	300
Ile Glu Thr Glu Leu Arg Pro Ser Asn Asn Leu Asn Leu Leu Ser Phe		
305	310	315
320		
Glu Asp Ser Thr Thr Gly Gly Val Gln Gln Lys Gln Ile Arg Glu His		
325	330	335
Glu Val Leu Ile His Val Glu Asp Glu Thr Trp Asp Pro Thr Leu Asp		
340	345	350
His Leu Ala Lys His Asp Gly Glu Asp Val Leu Gly Asn Lys Val Glu		
355	360	365
Arg Lys Glu Asp Gly Phe Glu Asp Gly Val Glu Asp Asn Lys Leu Lys		
370	375	380
Glu Asn Met Glu Arg Ala Cys Leu Met Ser Leu Asp Ile Thr Glu His		
385	390	395
400		
Glu Leu Gln Ile Leu Glu Gln Gln Ser Gln Glu Glu Tyr Leu Ser Asp		
405	410	415
Ile Ala Tyr Lys Ser Thr Glu His Leu Ser Pro Asn Asp Asn Glu Asn		
420	425	430
Asp Thr Ser Tyr Val Ile Glu Ser Asp Glu Asp Leu Glu Met Glu Met		
435	440	445
Leu Lys His Leu Ser Pro Asn Asp Asn Glu Asn Asp Thr Ser Tyr Val		
450	455	460
Ile Glu Ser Asp Glu Asp Leu Glu Met Glu Met Leu Lys Ser Leu Glu		
465	470	475
480		
Asn Leu Asn Ser Gly Thr Val Glu Pro Thr His Ser Lys Cys Leu Lys		
485	490	495
Met Glu Arg Asn Leu Gly Leu Pro Thr Lys Glu Glu Glu Asp Asp		

500	505	510
Glu Asn Glu Ala Asn Glu Gly Glu Glu Asp Asp Asp Lys Asp Phe Leu		
515	520	525
Trp Pro Ala Pro Asn Glu Glu Gln Val Thr Cys Leu Lys Met Tyr Phe		
530	535	540
Gly His Ser Ser Phe Lys Pro Val Gln Trp Lys Val Ile His Ser Val		
545	550	555
Leu Glu Glu Arg Arg Asp Asn Val Ala Val Met Ala Thr Gly Tyr Gly		
565	570	575
Lys Ser Leu Cys Phe Gln Tyr Pro Pro Val Tyr Val Gly Lys Ile Gly		
580	585	590
Leu Val Ile Ser Pro Leu Ile Ser Leu Met Glu Asp Gln Val Leu Gln		
595	600	605
Leu Lys Met Ser Asn Ile Pro Ala Cys Phe Leu Gly Ser Ala Gln Ser		
610	615	620
Glu Asn Val Leu Thr Asp Ile Lys Leu Gly Lys Tyr Arg Ile Val Tyr		
625	630	635
Val Thr Pro Glu Tyr Cys Ser Gly Asn Met Gly Leu Leu Gln Gln Leu		
645	650	655
Glu Ala Asp Ile Gly Ile Thr Leu Ile Ala Val Asp Glu Ala His Cys		
660	665	670
Ile Ser Glu Trp Gly His Asp Phe Arg Asp Ser Phe Arg Lys Leu Gly		
675	680	685
Ser Leu Lys Thr Ala Leu Pro Met Val Pro Ile Val Ala Leu Thr Ala		
690	695	700
Thr Ala Ser Ser Ser Ile Arg Glu Asp Ile Val Arg Cys Leu Asn Leu		
705	710	715
Arg Asn Pro Gln Ile Thr Cys Thr Gly Phe Asp Arg Pro Asn Leu Tyr		
725	730	735
Leu Glu Val Arg Arg Lys Thr Gly Asn Ile Leu Gln Asp Leu Gln Pro		
740	745	750
Phe Leu Val Lys Thr Ser Ser His Trp Glu Phe Glu Gly Pro Thr Ile		
755	760	765
Ile Tyr Cys Pro Ser Arg Lys Met Thr Gln Gln Val Thr Gly Glu Leu		
770	775	780
Arg Lys Leu Asn Leu Ser Cys Gly Thr Tyr His Ala Gly Met Ser Phe		
785	790	795
Ser Thr Arg Lys Asp Ile His His Arg Phe Val Arg Asp Glu Ile Gln		

805	810	815
Cys Val Ile Ala Thr Ile Ala Phe Gly Met Gly Ile Asn Lys Ala Asp		
820	825	830
Ile Arg Gln Val Ile His Tyr Gly Ala Pro Lys Asp Met Glu Ser Tyr		
835	840	845
Tyr Gln Glu Ile Gly Arg Ala Gly Arg Asp Gly Leu Gln Ser Ser Cys		
850	855	860
His Val Leu Trp Ala Pro Ala Asp Ile Asn Leu Asn Arg His Leu Leu		
865	870	875
Thr Glu Ile Arg Asn Glu Lys Phe Arg Leu Tyr Lys Leu Lys Met Met		
885	890	895
Ala Lys Met Glu Lys Tyr Leu His Ser Ser Arg Cys Arg Arg Gln Ile		
900	905	910
Ile Leu Ser His Phe Glu Asp Lys Gln Val Gln Lys Ala Ser Leu Gly		
915	920	925
Ile Met Gly Thr Glu Lys Cys Cys Asp Asn Cys Arg Ser Arg Leu Asp		
930	935	940
His Cys Tyr Ser Met Asp Asp Ser Glu Asp Thr Ser Trp Asp Phe Gly		
945	950	955
960		
Pro Gln Ala Phe Lys Leu Leu Ser Ala Val Asp Ile Leu Gly Glu Lys		
965	970	975
Phe Gly Ile Gly Leu Pro Ile Leu Phe Leu Arg Gly Ser Asn Ser Gln		
980	985	990
Arg Leu Ala Asp Gln Tyr Arg Arg His Ser Leu Phe Gly Thr Gly Lys		
995	1000	1005
Asp Gln Thr Glu Ser Trp Trp Lys Ala Phe Ser Arg Gln Leu Ile Thr		
1010	1015	1020
Glu Gly Phe Leu Val Glu Val Ser Arg Tyr Asn Lys Phe Met Lys Ile		
1025	1030	1035
1040		
Cys Ala Leu Thr Lys Lys Gly Arg Asn Trp Leu His Lys Ala Asn Thr		
1045	1050	1055
Glu Ser Gln Ser Leu Ile Leu Gln Ala Asn Glu Glu Leu Cys Pro Lys		
1060	1065	1070
Lys Phe Leu Leu Pro Ser Ser Lys Thr Val Ser Ser Gly Thr Lys Glu		
1075	1080	1085
His Cys Tyr Asn Gln Val Pro Val Glu Leu Ser Thr Glu Lys Lys Ser		
1090	1095	1100
Asn Leu Glu Lys Leu Tyr Ser Tyr Lys Pro Cys Asp Lys Ile Ser Ser		

1105	1110	1115	1120
Gly Ser Asn Ile Ser Lys Lys Ser Ile Met Val Gln Ser Pro Glu Lys			
1125	1130	1135	
Ala Tyr Ser Ser Ser Gln Pro Val Ile Ser Ala Gln Glu Gln Glu Thr			
1140	1145	1150	
Gln Ile Val Leu Tyr Gly Lys Leu Val Glu Ala Arg Gln Lys His Ala			
1155	1160	1165	
Asn Lys Met Asp Val Pro Pro Ala Ile Leu Ala Thr Asn Lys Ile Leu			
1170	1175	1180	
Val Asp Met Ala Lys Met Arg Pro Thr Thr Val Glu Asn Val Lys Arg			
1185	1190	1195	1200
Ile Asp Gly Val Ser Glu Gly Lys Ala Ala Met Leu Ala Pro Leu Leu			
1205	1210	1215	
Glu Val Ile Lys His Phe Cys Gln Thr Asn Ser Val Gln Thr Asp Leu			
1220	1225	1230	
Phe Ser Ser Thr Lys Pro Gln Glu Glu Gln Lys Thr Ser Leu Val Ala			
1235	1240	1245	
Lys Asn Lys Ile Cys Thr Leu Ser Gln Ser Met Ala Ile Thr Tyr Ser			
1250	1255	1260	
Leu Phe Gln Glu Lys Lys Met Pro Leu Lys Ser Ile Ala Glu Ser Arg			
1265	1270	1275	1280
Ile Leu Pro Leu Met Thr Ile Gly Met His Leu Ser Gln Ala Val Lys			
1285	1290	1295	
Ala Gly Cys Pro Leu Asp Leu Glu Arg Ala Gly Leu Thr Pro Glu Val			
1300	1305	1310	
Gln Lys Ile Ile Ala Asp Val Ile Arg Asn Pro Pro Val Asn Ser Asp			
1315	1320	1325	
Met Ser Lys Ile Ser Leu Ile Arg Met Leu Val Pro Glu Asn Ile Asp			
1330	1335	1340	
Thr Tyr Leu Ile His Met Ala Ile Glu Ile Leu Lys His Gly Pro Asp			
1345	1350	1355	1360
Ser Gly Leu Gln Pro Ser Cys Asp Val Asn Lys Arg Arg Cys Phe Pro			
1365	1370	1375	
Gly Ser Glu Glu Ile Cys Ser Ser Lys Arg Ser Lys Glu Glu Val			
1380	1385	1390	
Gly Ile Asn Thr Glu Thr Ser Ser Ala Glu Arg Lys Arg Arg Leu Pro			
1395	1400	1405	
Val Trp Phe Ala Lys Gly Ser Asp Thr Ser Lys Lys Leu Met Asp Lys			

1410	1415	1420
Thr Lys Arg Gly Gly Leu Phe Ser		
1425	1430	
<210> 19		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:		
Oligonucleotide		
<400> 19		
cgacatgatc tgatacatcg ttatgccatt		30
<210> 20		
<211> 29		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:		
Oligonucleotide		
<400> 20		
cattttataa taacgctgcg gacatctac		29
<210> 21		
<211> 1041		
<212> DNA		
<213> Arabidopsis thaliana		
<400> 21		
atgtttgagt ttttcgcttc aggaggaagg tcgcccacac aagaagctaa tgagccacca 60		
gttcccgattt acattgtgac ggatccgttt caacttcctg ctgatttcct aaacccttct 120		
cctgaaaaga aattggttat cggttttgac tttgagggtt ttgactctctt ccgacatggg 180		
aaactttgtt tcatgcagat tgcattctctt aatgcaatat acttggttga ttttcatcgaa 240		
ggtggagagg tgattatgaa agcgtgttgg cctgcactcg agtctaaat catcacgaaa 300		
gttatttcacg attgcaagcg tgacagttagt gctctataact tccagtttgg gataagattt 360		
cacaatgtt tggacactca gattgtttat tctctgtt aagaacaaga agggcggagg 420		
agacctctag atgattacat atcggttgc tcaactcctt ctgatccacg ttactgcgtt 480		
atatcctatg aagagaaaaga agaagttcgat gttctcatgc gccaggaccc aaagttttgg 540		
acatacaggc ctatgactga gctcatgatc cggcggactcg ctgtatgtt cggccatctt 600		
ctgtatctt atcacaaaaat gatggggaaat ctaaatcaggc ggtcaactatg gcatcttgca 660		
gttcgtgggtt ctttgcgttgc tgggtgttgc tgctgttgc atgtatgtt gtttgcgtt 720		
tggccaaaccg ttccatccat tccagtttgc ctcgtttaagg tcgtatgtc ttttgcgtt 780		
aagaaaaaaa gacgggttgc attagcttcg atgggttac tgattgttgc tggactttt 840		
aatgtggcag ataacacttgcg gtcagaagat caatgtcttgc aagaagagat cctgttgcgtt 900		
cttgcgttgc caccaggaaa gatggggacgt gtgttgcgttgc gggaaaggagc atcgtatctt 960		
gccatataagg aagcttgcgaa cgcggaaatt ctaatggag gggcaaggg tccacacttgc 1020		
aagggttagtc ttattccata g		1041

<210> 22

<211> 346

<212> PRT

<213> Arabidopsis thaliana

<400> 22

Met Phe Glu Phe Phe Ala Ser Gly Gly Arg Ser Pro Thr Gln Glu Ala
1 5 10 15

Asn Glu Pro Pro Val Pro Ile Tyr Ile Val Thr Asp Pro Phe Gln Leu
20 25 30

Pro Ala Asp Phe Leu Asn Pro Ser Pro Glu Lys Lys Leu Val Ile Gly
35 40 45

Phe Asp Cys Glu Gly Val Asp Leu Cys Arg His Gly Lys Leu Cys Ile
50 55 60

Met Gln Ile Ala Phe Ser Asn Ala Ile Tyr Leu Val Asp Val Ile Glu
65 70 75 80

Gly Gly Glu Val Ile Met Lys Ala Cys Lys Pro Ala Leu Glu Ser Asn
85 90 95

Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu
100 105 110

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
115 120 125

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
130 135 140

Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
145 150 155 160

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
165 170 175

Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
180 185 190

Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
195 200 205

Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
210 215 220

Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
225 230 235 240

Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
245 250 255

Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
260 265 270

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
275 280 285

Glu Asp Gln Cys Leu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
290 295 300

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
305 310 315 320

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
325 330 335

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
340 345

<210> 23

<211> 1049

<212> DNA

<213> Arabidopsis thaliana

<400> 23

accaaaggat taatttttat tttttgttt cagtaaaaga aatgtcatcg tcaaatttggaa 60
tcgacgacgc ttttacagag gaagagcttc tcgctatcgaa cgccatcgaa gcttcctaca 120
atttctcccg ttcttcttct tcttcttcct ctgctgctcc gaccgtacaa gctacaacct 180
ccgtccatgg ccacgaggag gatccaaatc aaatccccaa taatatccgt cgccaaattgc 240
ctcgttccat cacttcttct acatcttata aacgatttcc tctctcccg tgccgagcta 300
ggaattttcc agcaatgagg tttgggtgta ggattttgta tagcaagact gctactgagg 360
ttgataagcg agcaatgcag cttattaaag ttcttgatac caagagagat gaatctggaa 420
tagctttgt tggcttggat attgagtggaa gaccaagttt tagaaaagggt gttctcccg 480
ggaagggtgc gactgtccag atatgtgtat atagtaatta ttgtgatgtt atgcataattt 540
ttcattctgg tatccctcaa agtctccaaac atcttattga agattcaaca cttgtaaagg 600
taggtattgg aattgatggc gactctgtga agctttcca tgactatggaa gttagttatca 660
aagatgtga ggatcttca gatttagccaa accaaaaat tggtggagat aaaaaatggg 720
gccttgcctc actaactgag acacttggttt gcaaagagct cctgaagccaa aacagaatca 780
ggcttgggaa ctgggagttt tattctctgt caaagcagca gttacaatac gcagcaacgg 840
atgcttatgc ttcatggcat ctttacaagg ttcttaagga ccttcctgat gctgtcagtg 900
gctcataacg tgaaggagga agcttaaagg tttagctata accccaagag ttagcatcaa 960
atgatatgt acacctaatac tagtcaagta gatgcaattc ttgtgaatat tgtatctagt 1020
tctggccct ttaaccgtcc agaaaactag 1049

<210> 24

<211> 288

<212> PRT

<213> Arabidopsis thaliana

<400> 24

Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
1 5 10 15

Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
20 25 30

Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
35 40 45

His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
 50 55 60

Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
 65 70 75 80

Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
 85 90 95

Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
 100 105 110

Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
 115 120 125

Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
 130 135 140

Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
 145 150 155 160

Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
 165 170 175

His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
 180 185 190

Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
 195 200 205

Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
 210 215 220

Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
 225 230 235 240

Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
 245 250 255

Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
 260 265 270

His Leu Tyr Lys Val Leu Lys Asp Leu Pro Asp Ala Val Ser Gly Ser
 275 280 285

<210> 25
 <211> 22
 <212> DNA
 <213> Description of Artificial Sequence:
 Oligonucleotide

<400> 25
 ttcggaacca ccatcaaaca gg

<210> 26		
<211> 22		
<212> DNA		
<213> Description of Artificial Sequence:		
Oligonucleotide		
<400> 26		
ttgctgcaac tctctcaggg cc		22
<210> 27		
<211> 21		
<212> DNA		
<213> Description of Artificial Sequence:		
Oligonucleotide		
<400> 27		
tcaagctgttg cccgtctcac t		21
<210> 28		
<211> 16		
<212> DNA		
<213> Description of Artificial Sequence:		
Oligonucleotide		
Other n=a, c, g, or t		
<400> 28		
wgtgnagwan canaga		16
<210> 29		
<211> 27		
<212> DNA		
<213> Description of Artificial Sequence:		
Oligonucleotide		
<400> 29		
gctccggcca cataattcaa acaacac		27
<210> 30		
<211> 22		
<212> DNA		
<213> Description of Artificial Sequence:		
Oligonucleotide		
<400> 30		
ttcgaaaaca ttacctccga tc		22
<210> 31		
<211> 25		
<212> DNA		
<213> Description of Artificial Sequence:		
Oligonucleotide		
<400> 31		
ggctttgca ttggtatct actag		25

<210> 32
<211> 25
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 32
atgtcatcgt caaattggat cgacg

25

<210> 33
<211> 27
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 33
cgcttatcaa cctcagtagc agtcttg

27

<210> 34
<211> 24
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 34
ttatgagcca ctgacagcat cagg

24

<210> 35
<211> 1749
<212> DNA
<213> Arabidopsis thaliana

<400> 35
ATGGGTTTGG ATTCTAAAGA AGCTGATTTG GAGGTAATAA GAGATGAGAA ATCTGAAGCA
AACACTGTGT GTTTACATGC GTTTTCAGAT TTAACCTATG TGTCCTCTGT TGTGTTCTTA
TACCTACTCA AAAAATGCTA TAAACATGGT AGCTTGAAGG CAACAAAAAA GTTCCAAGCT
TTACAGTATC AAGTTCATCG AGTTCTAGCT AATAAACCTC AACCAAGGACC TGCTACTTTC
ATTATTAATT GTCTCACTTT ACTTCCTTTA TTTGGGGTAT ATGGTGAAGG CTTTAGTCAT
TTAGTTTATAT CAGCTCTTCG CCGCTCTCTT AAAACAGTAT CTGAACCAAC TAGTGAAGAA
GATATTTGGT TGGCGAGAAA GCTAGCTGCT CAGTTCTCC TTGCTACTGT TGTTGGATCT
TTAACCTTATG ATGAGAAGGT TATGGTCAT ACTCTTAGAG TGTTGATGT GAGGTTAACT
AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGTT TGCTTGTGGA
AATGCGTTTC TGGAACAATA CATTCTGAC TTGATCAAGT CGAAATCTT CATGACGGCT
GTGACTCTGT TAGAGCATT CTCTTCCGT TTCCCTGGAG AAACCTTTCT TCAACAAATG
GTTGAGGATA AAAATTCCA AGCTGCAGAG AGATGGGCTA CCTTCATGGG AAGGCCAAGT
TTATGCATTC TTGTTCAAGA GTATGGCTCA AGGAATATGC TAAAGCAGGC CTATAATATC
ATAAATAAGA ACTATCTACA GCATGACTTT CCCGAATTGT ATCACAAAGTG TAAAGAAAGT
GCTCTGAAGG TTCTAGCAGA AAAACATGTG TGGGATGTTG CTGAAATTAA GACAAAAGGT
GATAGACAGC TTCTGAAGTA TCTGGTATAC TTGGCAGGTGG AAGCTGGATA CTGGAGAAG
GTTGATGAAC TGTGCGATCG ATATTCACTT CAAGGGCTGC CAAAAGCACG AGAGGCTGAG
GTTGCTTTG TTGAAAAAAAG CTTTCTGGT CTCAACGATC TAGCTGTAGA AGATGTAGTT
TGGGGTGTG AAGTCAACGA GTTGAGAAAA GCAACTCTT TTCTGAAAGG ATGTAGAGTT
GTGGGTATTG ACTGTGAATG GAAACCTAAT TATATTAAG GCAGTAAACA GAACAAGGTT
TCAATCATGC AAATTGGATC TGATACCAAAT TTTTCATAT TGGACTTGAT AAAGCTTTAC
AATGACGCCCT CTGAAATTCTC GGACAACCTGC CTTAGTCACA TTTTGCAATC GAAGAGTACA
TTAAAGCTCG TCTCTCTGAC TGAGGATTAC CCTGATCATA AATTATCCTC AGGTTACAAT
TTTCATGTG ACATCAAGCA GTTGGCGCTT TCATATGGGG ATTTGAAATG TTTCGAGCGA
TACGACATGT TGCTAGACAT TCAAAATGTT TTTAATGAAC CATTGGTGG TTTCAGCAGGA
CTAACGAAGA AAATATTGGG AGTGTCTTG AACAAACAA GACGCAATAG CGACTGGAA

CAAAGGCCCTT TGAGCCAGAA TCAGCTTGAG TATGCTGCTC TTGATGCTGC AGTGTGATT	1620
CACATATTCG GCCATGTTCG CGATCATCCT CCACATGACA GTAGTCAGA GACAACCCAG	1680
TGGAAATCTC ACATTGTAAG TACCTCTTAT AAAAGCCCTT ATCTTCATC TGATAATTCA	1740
AGACGATAA	1749

<210> 36
 <211> 582
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 36			
Met Gly Leu Asp Ser Lys Glu Ala Asp Leu Glu Val Ile Arg Asp Glu			
1	5	10	
Lys Ser Glu Ala Asn Thr Val Cys Leu His Ala Phe Ser Asp Leu Thr			
20	25	30	
Tyr Val Ser Pro Val Val Phe Leu Tyr Leu Leu Lys Glu Cys Tyr Lys			
35	40	45	
His Gly Ser Leu Lys Ala Thr Lys Lys Phe Gln Ala Leu Gln Tyr Gln			
50	55	60	
Val His Arg Val Leu Ala Asn Lys Pro Gln Pro Gly Pro Ala Thr Phe			
65	70	75	80
Ile Ile Asn Cys Leu Thr Leu Leu Pro Leu Phe Gly Val Tyr Gly Glu			
85	90	95	
Gly Phe Ser His Leu Val Ile Ser Ala Leu Arg Arg Phe Phe Lys Thr			
100	105	110	
Val Ser Glu Pro Thr Ser Glu Glu Asp Ile Cys Leu Ala Arg Lys Leu			
115	120	125	
Ala Ala Gln Phe Phe Leu Ala Thr Val Gly Gly Ser Leu Thr Tyr Asp			
130	135	140	
Glu Lys Val Met Val His Thr Leu Arg Val Phe Asp Val Arg Leu Thr			
145	150	155	160
Ser Ile Asp Glu Ala Leu Ser Ile Ser Glu Val Trp Gln Arg Tyr Gly			
165	170	175	
Phe Ala Cys Gly Asn Ala Phe Leu Glu Gln Tyr Ile Ser Asp Leu Ile			
180	185	190	
Lys Ser Lys Ser Phe Met Thr Ala Val Thr Leu Leu Glu His Phe Ser			
195	200	205	
Phe Arg Phe Pro Gly Glu Thr Phe Leu Gln Gln Met Val Glu Asp Lys			
210	215	220	
Asn Phe Gln Ala Ala Glu Arg Trp Ala Thr Phe Met Gly Arg Pro Ser			
225	230	235	240

Leu Cys Ile Leu Val Gln Glu Tyr Gly Ser Arg Asn Met Leu Lys Gln
 245 250 255
 Ala Tyr Asn Ile Ile Asn Lys Asn Tyr Leu Gln His Asp Phe Pro Glu
 260 265 270
 Leu Tyr His Lys Cys Lys Glu Ser Ala Leu Lys Val Leu Ala Glu Lys
 275 280 285
 Ala Cys Trp Asp Val Ala Glu Ile Lys Thr Lys Gly Asp Arg Gln Leu
 290 295 300
 Leu Lys Tyr Leu Val Tyr Leu Ala Val Glu Ala Gly Tyr Leu Glu Lys
 305 310 315 320
 Val Asp Glu Leu Cys Asp Arg Tyr Ser Leu Gln Gly Leu Pro Lys Ala
 325 330 335
 Arg Glu Ala Glu Val Ala Phe Val Glu Lys Ser Phe Leu Arg Leu Asn
 340 345 350
 Asp Leu Ala Val Glu Asp Val Val Trp Val Asp Glu Val Asn Glu Leu
 355 360 365
 Arg Lys Ala Thr Ser Phe Leu Glu Gly Cys Arg Val Val Gly Ile Asp
 370 375 380
 Cys Glu Trp Lys Pro Asn Tyr Ile Lys Gly Ser Lys Gln Asn Lys Val
 385 390 395 400
 Ser Ile Met Gln Ile Gly Ser Asp Thr Lys Ile Phe Ile Leu Asp Leu
 405 410 415
 Ile Lys Leu Tyr Asn Asp Ala Ser Glu Ile Leu Asp Asn Cys Leu Ser
 420 425 430
 His Ile Leu Gln Ser Lys Ser Thr Leu Lys Leu Val Ser Leu Thr Glu
 435 440 445
 Asp Tyr Pro Asp His Lys Leu Ser Ser Gly Tyr Asn Phe Gln Cys Asp
 450 455 460
 Ile Lys Gln Leu Ala Leu Ser Tyr Gly Asp Leu Lys Cys Phe Glu Arg
 465 470 475 480
 Tyr Asp Met Leu Leu Asp Ile Gln Asn Val Phe Asn Glu Pro Phe Gly
 485 490 495
 Gly Leu Ala Gly Leu Thr Lys Lys Ile Leu Gly Val Ser Leu Asn Lys
 500 505 510
 Thr Arg Arg Asn Ser Asp Trp Glu Gln Arg Pro Leu Ser Gln Asn Gln
 515 520 525
 Leu Glu Tyr Ala Ala Leu Asp Ala Ala Val Leu Ile His Ile Phe Arg
 530 535 540

His Val Arg Asp His Pro Pro His Asp Ser Ser Ser Glu Thr Thr Gln
545 550 555 560

Trp Lys Ser His Ile Val Ser Thr Ser Tyr Lys Ser Pro Tyr Leu Ser
565 570 575

Ser Asp Asn Ser Arg Arg
580

<210> 37
<211> 1518
<212> DNA
<213> *Arabidopsis thaliana*

<400> 37

ATGGAGACCA	ATCTAAAGAT	CTATCTAGTT	TCATCCACCG	ACTCGTCCGA	GTTCACTCAC	60
CTGAAATGGT	CTTCACTCG	TTCTACGATC	ATCGCCTAG	ACGCCAATG	GAAGCCACAA	120
CACTCCAATA	CCTCGTCGTT	TCCGACCGTC	ACTCTCC	AAAGTCGCATG	CCGACTCAGT	180
CACGCCACGG	ATGCTCTCGGA	TGTCTTCCTC	ATTGATTGTA	GTTCGATTCA	TCTTCCATCG	240
GTGTTGGGAGC	TGTTGAATGA	TATGTTCTGT	TCGCCGATG	TTCTGAAACT	AGGGTTTGGG	300
TTTAAACAGG	ATTGGTTTA	CTTGTCTTCG	ACATTTACTC	AACATGGATG	TGAAGGTGGA	360
TTCCAAGAGG	TGAAACAATA	CTTGGATATT	ACAAGCATAT	ACAATTATCT	GCAACATAAG	420
CGGTTTGGGA	GAAAGGCGCC	AAAGGATATC	AAGAGCTTGG	CTGCTATATG	TAAGGAAATG	480
CTGGACATCT	CTCTCTCAA	GGAACTTCAA	TGTAGTGATT	GGTCATATCG	TCCCTTACA	540
GAAGAACAGA	AACTATACCC	TGCCACAGAT	GCTCACTGCC	TGCTCCAGAT	ATTCGATGTA	600
TTTGAGGCGC	ATCTGTTGA	AGGAATCACA	GTGCAAGATC	TTAGAGTGT	AAATGTTGGC	660
TTACAAAGAAA	TTCTGACTGA	ATCGGACTAT	AGCAGTAAGA	TTGTCACAGT	CAAACTTGC	720
AAGGCTACAG	ATGTAATCAG	ATCAATGTGG	GAAAATGGTC	AAAACATAGC	CAATGGAGTG	780
GTTCAGAAAGAA	AAACAGACACT	AAACACGATG	CCAATGGATG	AGAATTGTT	GAAGATTGTC	840
AGGAAGTTG	GAGAACGGAT	CCTGTTGAAG	GAGTCTGATC	TTCTACAAA	GAAACTTAAG	900
AAGAAAACAA	GAAGACGTGT	CGCCTCAAGC	ACTATGAACA	CAAATAACCA	GTGTTCTGT	960
TCTGCGGACT	GGCAAGGTCC	ACCGCCATGG	GACTCATTT	TAGGCGGTGA	TGGCTGCCCT	1020
AAATTCTAT	TGGATGTGAT	GGTTGAAGGT	TTGGCGAAC	ATCTACGTTG	TGTGGGGATT	1080
GATGCTGCAA	TCCCACACTC	AAAGAAGCCG	GATTCAAGGG	AGTTGCTTGA	TCAAGCATTC	1140
AAAGAGAACAA	GAGTTCTATT	AAACAAGAGAT	ACAAAATTGT	TGAGACACCA	GGATTTGGCA	1200
AAGCATCAA	TATATCGACT	AAAGAGTCTT	CTTAAAAATG	AGCAGCTACT	TGAGGTGATA	1260
GAGACTTCC	AGCTAAAGAT	CAGCGGAAT	CAGCTGATGT	CCAGATGTAC	GAAGTGCAAT	1320
GGGAAATTAA	TTCAGAAACC	TCTAAGCATT	GAAGAAGCTA	TTGAAGCAGC	AAAGGGTTTC	1380
CAAAGAATAC	CCAACTGCTT	ATTTAACAAA	AATTTAGAGT	TTTGGCACTG	CATGAACTGC	1440
CATCAACTAT	ACTGGGAGGG	AACTCAGTAT	CATAACCGAG	TCCAGAAAGTT	CATGGAAGTA	1500
TGCAAGTGA	GTGAGTGA					1518

<210> 38
<211> 505
<212> PRT
<213> *Arabidopsis thaliana*

<400> 38

Met	Glu	Thr	Asn	Leu	Lys	Ile	Tyr	Leu	Val	Ser	Ser	Thr	Asp	Ser	Ser
1				5				10				15			

Glu Phe Thr His Leu Lys Trp Ser Phe Thr Arg Ser Thr Ile Ile Ala
20 25 30

Leu Asp Ala Glu Trp Lys Pro Gln His Ser Asn Thr Ser Ser Phe Pro
35 40 45

Thr Val Thr Leu Leu Gln Val Ala Cys Arg Leu Ser His Ala Thr Asp

50	55	60
Val Ser Asp Val Phe Leu Ile Asp Leu Ser Ser Ile His Leu Pro Ser		
65	70	75
Val Trp Glu Leu Leu Asn Asp Met Phe Val Ser Pro Asp Val Leu Lys		
85	90	95
Leu Gly Phe Arg Phe Lys Gln Asp Leu Val Tyr Leu Ser Ser Thr Phe		
100	105	110
Thr Gln His Gly Cys Glu Gly Phe Gln Glu Val Lys Gln Tyr Leu		
115	120	125
Asp Ile Thr Ser Ile Tyr Asn Tyr Leu Gln His Lys Arg Phe Gly Arg		
130	135	140
Lys Ala Pro Lys Asp Ile Lys Ser Leu Ala Ala Ile Cys Lys Glu Met		
145	150	155
160		
Leu Asp Ile Ser Leu Ser Lys Glu Leu Gln Cys Ser Asp Trp Ser Tyr		
165	170	175
Arg Pro Leu Thr Glu Glu Gln Lys Leu Tyr Ala Ala Thr Asp Ala His		
180	185	190
Cys Leu Leu Gln Ile Phe Asp Val Phe Glu Ala His Leu Val Glu Gly		
195	200	205
Ile Thr Val Gln Asp Leu Arg Val Ile Asn Val Gly Leu Gln Glu Ile		
210	215	220
Leu Thr Glu Ser Asp Tyr Ser Ser Lys Ile Val Thr Val Lys Leu Cys		
225	230	235
240		
Lys Ala Thr Asp Val Ile Arg Ser Met Ser Glu Asn Gly Gln Asn Ile		
245	250	255
Ala Asn Gly Val Val Pro Arg Lys Thr Thr Leu Asn Thr Met Pro Met		
260	265	270
Asp Glu Asn Leu Leu Lys Ile Val Arg Lys Phe Gly Glu Arg Ile Leu		
275	280	285
Leu Lys Glu Ser Asp Leu Leu Pro Lys Lys Leu Lys Lys Lys Thr Arg		
290	295	300
Arg Arg Val Ala Ser Ser Thr Met Asn Thr Asn Lys Gln Leu Val Cys		
305	310	315
320		
Ser Ala Asp Trp Gln Gly Pro Pro Pro Trp Asp Ser Ser Leu Gly Gly		
325	330	335
Asp Gly Cys Pro Lys Phe Leu Leu Asp Val Met Val Glu Gly Leu Ala		
340	345	350
Lys His Leu Arg Cys Val Gly Ile Asp Ala Ala Ile Pro His Ser Lys		

355 360 365

Lys Pro Asp Ser Arg Glu Leu Leu Asp Gln Ala Phe Lys Glu Asn Arg
370 375 380

Val Leu Leu Thr Arg Asp Thr Lys Leu Leu Arg His Gln Asp Leu Ala
385 390 395 400

Lys His Gln Ile Tyr Arg Val Lys Ser Leu Leu Lys Asn Glu Gln Leu
405 410 415

Leu Glu Val Ile Glu Thr Phe Gln Leu Lys Ile Ser Gly Asn Gln Leu
420 425 430

Met Ser Arg Cys Thr Lys Cys Asn Gly Lys Phe Ile Gln Lys Pro Leu
435 440 445

Ser Ile Glu Glu Ala Ile Glu Ala Ala Lys Gly Phe Gln Arg Ile Pro
450 455 460

Asn Cys Leu Phe Asn Lys Asn Leu Glu Phe Trp Gln Cys Met Asn Cys
465 470 475 480

His Gln Leu Tyr Trp Glu Gly Thr Gln Tyr His Asn Ala Val Gln Lys
485 490 495

Phe Met Glu Val Cys Lys Leu Ser Glu
500 505

PB/5-31481A

1

3

4

28